

Db 61 QYRVIDFKRKGIPGRVATIEYDPNRSANIALINADGK--YIIAAKGLVGGTIYS 118
 QY 121 GAADTKVGNALPLQNPVGTVVHNIETKPGQIARSAGASAQVLGKGGKVLRLRS 180
 Db 119 GAADTKVGNALPLQNPVGTVVHNIETKPGQIARSAGASAQVLGKGGKVLRLRS 178
 QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGGR 240
 Db 179 GEVRMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGGR 238
 QY 241 APIGRSPSPWGKPTLGKKTGRGKSSDKLIVRGKKK 279
 Db 239 APIGRSPSPWGKPTLGKKTGRGKSSDKLIVRGKKK 277

RESULT 15

ADSA44623 standard; protein; 277 AA.

XX AC ADS44623;
 XX DT 02-DEC-2004 (first entry)
 XX DE Bacterial polypeptide #23053.
 XX KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.

XX OS Bacteria.

XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX PA (CAOY/) CAO Y.
 XX PA (HINK/) HINKLE G J.
 XX PA (SLAT/) SLATER S C.
 XX PA (CHEN/) CHEN X.
 XX PA (GOLD/) GOLDMAN B S.

XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX DR WPI; 2004-061375/06.

XX PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.

XX PS Claim 1; SEQ ID NO 23053; 122pp; English.

XX CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,

CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 277 AA;

Query Match 79.9%; Score 1163; DB 8; Length 277;

Best Local Similarity 79.9%; Pred. No. 6.8e-108;

Matches 223; Conservative 19; Mismatches 35; Indels 2; Gaps 1;

QY 1 MAIKKYKPTNGRRNMTSLDPABITKTTPEKSLKLLPLPKAGRNQOKLTVRHGGGHR 60
 Db 1 MAIKKYKPSNGRRGNTTSDFAEITTDKPEKSLLAFLHKKGGRRNQOKLTVRHGGGHR 60
 QY 61 QYRVIDFKRKGIPGRVATIEYDPNRSANIALINADGK--YIIAAKGLVGGTIYS 120
 Db 61 QYRVIDFKRKGIPGRVATIEYDPNRSANIALINADGK--YIIAAKGLVGGTIYS 118
 QY 121 GAADTKVGNALPLQNPVGTVVHNIETKPGQIARSAGASAQVLGKGGKVLRLRS 180
 Db 119 GPEADIKVGNALPLQNPVGTVVHNIETKPGQIARSAGASAQVLGKGGKVLRLRS 178
 QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGGR 240
 Db 179 GEVRMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGGR 238
 QY 241 APIGRSPSPWGKPTLGKKTGRGKSSDKLIVRGKKK 279
 Db 239 APIGRSPSPWGKPTLGKKTGRGKSSDKLIVRGKKK 277

Search completed: June 9, 2005, 16:04:23

Job time : 165 secs

PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
PI Duesurget O, Chetouani F, Glaser P, Kunst F, Cossart P;
PI Daniela J, Goebel W, Krefit J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX
XX WPI; 2002-010914/01.
DR
XX
XX Genomic sequence for *Listeria monocytogenes*, useful e.g. for treatment
PT and prevention of *Listeria* and related bacterial infections, and related
PT polypeptides.
XX
XX Claim 6; SEQ ID NO 2071; 192pp; French.
PS
XX
XX The present invention relates to the genome sequence of *Listeria*
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in *L.*
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of *L. monocytogenes* and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate *L. monocytogenes*-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by *L.*
CC monocytogenes and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 277 AA;

Query Match 82.6%; Score 1203; DB 5; Length 277;
Best Local Similarity 82.4%; Pred. No. 6.5e-112;
Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;

Qy 1 MAIKKYPITNGRRNMTSLDPAETTKTPKSLKPLPKKAGRNQKLTVRHHGGGHR 60
Db 1 MAIKKYPITNGRRNMTSSDPAETTTTPKSLRLPLKPKKAGRNQKLTVRHHGGGHR 60

Qy 61 QYRVDFKRNKDGINAKVDSIQYDPNRSANIALVYADGKRIYHCIAPKGLEVGQIVES 120
Db 61 QYRVDFKRNKDGIPRVATIEYDPNRSANIALINYADGKR--YIIAAGLEVGQTIYS 118

Qy 121 GAEDATKGNALPLQNIPIVGTIVNIELKPKGQIARSAGASQVTKGKYYLILRS 180
Db 119 GAEDAIKVGNALELKDIPVGTIVNIELKPKGQIARSAGTSQVTLGKGGYYLILRS 178

Qy 181 GEVRMILSTRATIGQVGNLQHELVNKGKRSWKGRIPTRVGSVWPNNDHPHGGEGR 240
Db 179 GEVRMILATCRATIGQVNGEHELINTGKGRSWMGRPTVRGSVWPNNDHPHGGEGR 238

Qy 241 APIGRSPMSPWGKPTLGKTRRGGKSSDKLIVGRKKK 279
Db 239 APIGRSPMSPWGKPTLGKTRKKNNSDKPIVRRKKK 277

RESULT 14
ABU32542
ID ABU32542 standard; protein; 277 AA.

XX
AC ABU32542;
XX
XX 19-JUN-2003 (first entry)
DT
XX Protein encoded by *Prokaryotic essential gene #18069*.
DE
XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX *Listeria monocytogenes*.
OS
XX WO200277183-A2.
XX
XX 03-OCT-2002.
PD
XX
XX 21-MAR-2002; 2002WO-US009107.
PF
XX
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
FA
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR N-PSDB; ACA36412.
DR
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 60466; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 277 AA;

Query Match 82.6%; Score 1203; DB 6; Length 277;
Best Local Similarity 82.4%; Pred. No. 6.5e-112;
Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;

Qy 1 MAIKKYPITNGRRNMTSLDPAETTKTPKSLKPLPKKAGRNQKLTVRHHGGGHR 60
Db 1 MAIKKYPITNGRRNMTSSDPAETTTTPKSLRLPLKPKKAGRNQKLTVRHHGGGHR 60
Qy 61 QYRVDFKRNKDGINAKVDSIQYDPNRSANIALVYADGKRIYHCIAPKGLEVGQIVES 120

CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 CC Sequence 277 AA;

Query Match 94.3%; Score 1373; DB 6; Length 277;
 Best Local Similarity 93.3%; Pred. No. 5.7e-129;
 Matches 262; Conservative 11; Mismatches 4; Indels 2; Gaps 1;
 QY 1 MALKKYKPTNGRRNMTSLDFAEITKTTPKSLKLPKAGRNNOGKLTVRHHGGGHR 60
 DB 1 MALKKYKPTNGRRNMTSLDFAEITKTTPKSLKLPKAGRNNOGKLTVRHHGGGHR 60
 QY 61 QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVS 120
 DB 61 QYRVIDFKRNKDGIIAKVDSIQYDPNRSANIALLVYADGKR--YIIAPKGLQVGQTVS 118
 QY 121 GAEDATKVGNALPLQNPVGTVVHNIELPKGKGQIARSAGASQVLGKGGKVLRLRS 180
 DB 119 GAEDATKVGNALPLQNPVGTVVHNIELPKGKGQIARSAGASQVLGKGGKVLRLRS 178
 QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIPTVRGSMVNPNDHPHGGGEGR 240
 DB 179 GEVRMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIPTVRGSMVNPNDHPHGGGEGR 238
 QY 241 APIGRSPSPWGKPTLGKTRRGKSSDKLIVRGRKK 279
 DB 239 APIGRSPSPWGKPTLGKTRRGKSSDKLIVRGRKK 277

RESULT 13
 ABB49366
 ID ABB49366 standard; protein; 277 AA.
 AC ABB49366;
 XX
 DT 05-FEB-2002 (first entry)
 XX
 DE Listeria monocytogenes protein #2070.
 XX
 KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KW vitamin B12; bacterial infection; disease.
 XX
 OS Listeria monocytogenes.
 XX
 PN WO2001/77335-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 11-APR-2001; 2001WO-FR001118.
 XX
 PR 11-APR-2000; 2000FR-00004629.
 XX
 PA (INSP) INST PASTEUR.
 XX

RESULT 12
 ABU42626
 ID ABU42626 standard; protein; 277 AA.
 AC ABU42626;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #28153.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Staphylococcus epidermidis.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX

(ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA46496.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 70550; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of

XX OS Staphylococcus epidermidis.
XX PN US2004147734-A1.
XX XX 29-JUL-2004.
XX PF 01-DEC-2003; 2003US-00724972.
XX PR 08-NOV-1997; 97US-0064964P.
XX PR 13-AUG-1998; 98US-00134001.
XX PR 29-NOV-1999; 99US-00450969.
XX XX (DOUC/) DOUCETTE-STAMM L.
XX PA (BUSH/) BUSH D.
XX PI Doucette-Stamm L, Bush D;
XX DR WPI; 2004-580138/56.
XX DR N-PSDB; ADS03304.
XX XX New isolated polypeptide and encoding nucleic acid derived from
PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or
PT treating an S. epidermidis bacterial infection.
XX XX
XX PS Claim 17; SEQ ID NO 6371; 741pp; English.
XX CC The invention describes an isolated nucleic acid comprising a nucleotide
CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:
CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any
CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as
CC given in the specification. Also described are: a recombinant expression
CC vector; a call comprising a recombinant expression vector of (1);
CC producing an S. epidermidis polypeptide; an isolated nucleic acid
CC comprising a nucleotide sequence of at least 8 nucleotides in length; a
CC vaccine composition for prevention or treatment of an S. epidermidis
CC infection, comprising a nucleic acid cited above and a carrier; treating
CC a subject for S. epidermidis infection; a recombinant or substantially
CC pure preparation of an S. epidermidis polypeptide or its fragment; a
CC vaccine composition for prevention or treatment of an S. epidermidis
CC infection; detecting the presence of a Staphylococcus nucleic acid in a
CC sample; a computer readable medium having recorded in it the nucleotide
CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based
CC system for identifying fragments of the Staphylococcus genome of
CC commercial importance; a computer based system for identifying fragments
CC of the Staphylococcus plasmids of commercial importance; identifying
CC commercially important nucleic acid fragments of the Staphylococcus
CC genome and/or plasmids; and identifying an expression modulating fragment
CC of the Staphylococcus genome and/or plasmids. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of an Staphylococcus epidermidis bacterial
CC infection. This is the amino acid sequence of a S. epidermidis protein of
CC the invention.
XX XX
XX SQ Sequence 279 AA;
Query Match 94.4%; Score 1375; DB 8; Length 279;
Best Local Similarity 93.5%; Pred. No. 3.6e-129;
Matches 261; Conservative 12; Mismatches 4; Indels 2; Gaps 1;
QY 1 MATKKYKPIINGRRNMTSLDFAITKTTPEKSLKLPKPKAGRNNOGKLVRRHGGGSHKR 60
DB 3 MAUKKYKPIINGRRNMTTLDFAITKTTPEKSLQPLPKRAGRNNOGKLVRRHGGGSHKR 62
QY 61 QYRVDFKRNKGIDINAKVDSIQDPNRSANIALVYVADGKRYTHCTAPKGLVGVQIVES 120
DB 63 QYRVDFKRNKGITAKVDSIQDPNRSANIALVYVADGKRYTHCTAPKGLVGVQIVES 120
QY 121 GABADTKVGNALPLQNIPIVGTVVHNIETLKPCKGGQIARSAGASQVLPKGGKVVILRLRS 180
DB 121 GABADTKVGNALPLQNIPIVGTVVHNIETLKPCKGGQIARSAGASQVLPKGGKVVILRLRS 180
QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRSRWKGIPTVRGSMVNPNDHPHGGGEGR 240

DB 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRSRWKGIPTVRGSMVNPNDHPHGGGEGR 240
QY 241 APIGRSPSPMPGWKPTLGKKTTRGKSSDKLIVRGRKKK 279
DB 241 APIGRSPSPMPGWKPTLGKKTTRGKSSDKLIVRGRKKK 279
RESULT 11
ABJ19022
ID ABJ19022 standard; protein; 277 AA.
XX AC ABJ19022;
XX DT 06-MAR-2003 (first entry)
XX DE Pathogen specific antigen related staphylococcal protein SEQ ID No 271.
XX KW Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KW autoimmune disease; HIV; hepatitis.
XX OS Staphylococcus sp.
XX PN WO200259148-A2.
XX PD 01-AUG-2002.
XX PF 21-JAN-2002; 2002WO-EP000546.
XX PR 26-JAN-2001; 2001AT-00000130.
XX PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX PI Meinke A, Nagy E, Von Ahlsen U, Klade C, Henics T, Zauner W;
PI Minh DB, Vytvytska O, Btz H, Dryla A, Weichhart T, Hafner M;
PI Tempelmaier B;
XX DR WPI; 2003-075410/07.
XX PT Identifying, isolating and producing hyperimmune serum-reactive antigens
PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.
XX PS Example 7; Page 199; 252pp; English.
XX CC The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens are
CC used in a vaccine, comprises providing antibody preparation from a plasma
CC pool of a type of animal, or individual sera with antibodies against the
CC specific pathogen, tumour, allergen, tissue or host prone to auto-
CC immunity. The hyperimmune serum-reactive antigens comprising any of the
CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against S. aureus or S. epidermidis. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against S. aureus or S. epidermidis. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX SQ Sequence 277 AA;
Query Match 94.3%; Score 1373; DB 6; Length 277;
Best Local Similarity 93.9%; Pred. No. 5.7e-129;
Matches 262; Conservative 11; Mismatches 4; Indels 2; Gaps 1;

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 277 AA;

Query Match 94.8%; Score 1380; DB 6; Length 277;
 Best Local Similarity 94.3%; Pred. No. 1.1e-129;
 Matches 263; Conservative 11; Mismatches 3; Indels 2; Gaps 1;
 QY 1 MAIKKYKPTITNGRRNMTSLDFABITKTTPKSLKLPKPKAGRNNOGKLTVRHHGGGHR 60
 DB 1 MALKKYKPTITNGRRNMTSLDFABITKTTPKSLKLPKPKAGRNNOGKLTVRHHGGGHR 60
 QY 61 QYRVIDFKRNKGINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVS 120
 DB 61 QYRVIDFKRNKGITAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVS 118
 QY 121 GAADTKVGNALPLQNIPIVGTVIHNIELPKGKGQIARSAGASQVLGKGGKVLRLRS 180
 DB 119 GAADTKVGNALPLQNIPIVGTVIHNIELPKGKGQIARSAGASQVLGKGGKVLRLRS 178
 QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIPTVRGSMVNPNDHPHGGGEGR 240
 DB 179 GEVRMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIPTVRGSMVNPNDHPHGGGEGR 238
 QY 241 APIGRSPSPMPGKPTLGKTRGKSSDKLIVRGKKK 279
 DB 239 APIGRSPSPMPGKPTLGKTRGKSSDKLIVRGKKK 277

RESULT 9
 ABP38415
 ID ABP38415 standard; protein; 279 AA.
 AC ABP38415;
 XX
 DT 24-JUL-2002 (first entry)
 DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3260.
 XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 KW Staphylococcus epidermidis; gene therapy.
 KW antibacterial; gene therapy.
 XX
 OS Staphylococcus epidermidis.

XX US6380370-B1.
 PN 30-APR-2002.
 XX 13-AUG-1998; 98US-00134001.
 XX 14-AUG-1997; 97US-0055779P.
 PR 08-NOV-1997; 97US-0064964P.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 XX Doucette-Stamm LA, Bush D;
 PI WPI; 2002-381255/41.
 XX N-PSDB; ABN90960.
 PT Novel isolated nucleic acid encoding a Staphylococcus epidermis
 PT polypeptide, useful for diagnosing and treating bacterial infections.
 PS Disclosure; SEQ ID NO 3260; 267pp; English.
 CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 CC given in ABP35124 to ABP37960. The *S. epidermidis* sequences have
 CC antibacterial activity and can be used in gene therapy. The sequences can
 CC also be used in the diagnosis and treatment of bacterial infections,
 CC particularly *S. epidermidis* infections. The sequences can be used to
 CC screen for compounds able to interfere with the *S. epidermidis* life cycle
 CC or inhibit *S. epidermidis* infection. N.B. The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from the USPTO web site
 XX Sequence 279 AA;

Query Match 94.4%; Score 1375; DB 5; Length 279;
 Best Local Similarity 93.5%; Pred. No. 3.6e-129;
 Matches 261; Conservative 12; Mismatches 4; Indels 2; Gaps 1;
 QY 1 MAIKKYKPTITNGRRNMTSLDFABITKTTPKSLKLPKPKAGRNNOGKLTVRHHGGGHR 60
 DB 3 MALKKYKPTITNGRRNMTSLDFABITKTTPKSLKLPKPKAGRNNOGKLTVRHHGGGHR 62
 QY 61 QYRVIDFKRNKGINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVS 120
 DB 63 QYRVIDFKRNKGITAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVS 120
 QY 121 GAADTKVGNALPLQNIPIVGTVIHNIELPKGKGQIARSAGASQVLGKGGKVLRLRS 180
 DB 121 GAADTKVGNALPLQNIPIVGTVIHNIELPKGKGQIARSAGASQVLGKGGKVLRLRS 180
 QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIPTVRGSMVNPNDHPHGGGEGR 240
 DB 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIPTVRGSMVNPNDHPHGGGEGR 240
 QY 241 APIGRSPSPMPGKPTLGKTRGKSSDKLIVRGKKK 279
 DB 241 APIGRSPSPMPGKPTLGKTRGKSSDKLIVRGKKK 279

RESULT 10
 ADS07076
 ID ADS07076 standard; protein; 279 AA.
 AC ADS07076;
 XX
 DT 04-NOV-2004 (first entry)
 DE Staphylococcus epidermis polypeptide seqid 6371.
 XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 KW Staphylococcus epidermidis; gene therapy.
 KW antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;
 KW recombinant expression vector; infection; computer readable medium;
 KW computer based system.

CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 277 AA;

Query Match 97.0%; Score 1412; DB 6; Length 277;
Best Local Similarity 98.2%; Pred. No. 6.9e-133;
Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
QY 1 MAIKKYPITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
DB 1 MAIKKYPITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
QY 61 QYRVDFPRKNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVS 120
DB 61 QYRVDFPRKNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVS 118
QY 121 GAADTKVGNALPLQNIPTVGTVVHNIELKPGKGQIARSAGASAOVLGKGGKYLIRLS 180
DB 119 GAADIKVGNALPLQNIPTVGTVVHNIELKPGKGQIARSAGASAOVLGKGGKYLIRLS 178
QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGKRSWKGIPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVRMILSTCRATIGQVGNLQHELNVNKGKRSWKGIPTVRGSMVNPNDHPHGGGEGR 238
QY 241 APIGRSPSPMSWGKPTLGKTRRGKSSDKLIVGRKKK 279
DB 239 APIGRSPSPMSWGKPTLGKTRRGKSSDKLIVGRKKK 277

RESULT 7

ABM72939
ID ABM72939 standard; protein; 277 AA.

XX AC ABM72939;

XX 20-NOV-2003 (first entry)

XX Staphylococcus aureus protein #2179.

XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX enzymatic assay; antibiotic target.

XX Staphylococcus aureus.

XX WO200294868-A2.

XX 28-NOV-2002.

XX 27-MAR-2002; 2002WO-IB002637.

XX 27-MAR-2001; 2001GB-00007661.

XX (CHIR-) CHIRON SPA.

XX Masignani V, Mora M, Scarselli M;

XX WPI; 2003-120786/11.

XX N-PSDB; ACF74499.

XX New Staphylococcus aureus protein, useful as a vaccine for treating or
XX preventing Staphylococcal infection, specifically an infection caused by
XX S. aureus, e.g. sepsis.

XX Claim 1; SEQ ID NO 4358; 49pp; English.

XX The invention relates to novel genes and encoded proteins from

XX Staphylococcus aureus. A composition comprising the S. aureus protein, a
XX nucleic acid encoding the protein, or an antibody to the protein, is
XX useful as a pharmaceutical, particularly as a vaccine for treating or
XX preventing infection due to Staphylococcus bacteria, specifically an

CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus proteins of the invention

XX SQ Sequence 277 AA;

Query Match 97.0%; Score 1412; DB 6; Length 277;
Best Local Similarity 98.2%; Pred. No. 6.9e-133;
Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
QY 1 MAIKKYPITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
DB 1 MAIKKYPITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
QY 61 QYRVDFPRKNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVS 120
DB 61 QYRVDFPRKNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVS 118
QY 121 GAADTKVGNALPLQNIPTVGTVVHNIELKPGKGQIARSAGASAOVLGKGGKYLIRLS 180
DB 119 GAADIKVGNALPLQNIPTVGTVVHNIELKPGKGQIARSAGASAOVLGKGGKYLIRLS 178
QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGKRSWKGIPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVRMILSTCRATIGQVGNLQHELNVNKGKRSWKGIPTVRGSMVNPNDHPHGGGEGR 238
QY 241 APIGRSPSPMSWGKPTLGKTRRGKSSDKLIVGRKKK 279
DB 239 APIGRSPSPMSWGKPTLGKTRRGKSSDKLIVGRKKK 277

RESULT 8

ABU43554
ID ABU43554 standard; protein; 277 AA.

XX AC ABU43554;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #29081.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Staphylococcus haemolyticus.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 08-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX WPI; 2003-0299926/02.

XX N-PSDB; ACA47424.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX Claim 25; SEQ ID NO 71478; 1766pp; English.

DE Pathogen specific antigen related staphylococcal protein SEQ ID No 222.
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KW autoimmune disease; HIV; hepatitis.
XX
XX Staphylococcus sp.
OS
XX WO200259148-A2.
XX
XX 01-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-EP000546.
XX
XX 26-JAN-2001; 2001AT-00000130.
XX
XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
XX Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;
PI Minh DB, Vytvytska O, Btz H, Dryla A, Weichhart T, Hafner M;
PI Tempelmaier B;
XX
XX WPI; 2003-075410/07.
XX
XX Identifying, isolating and producing hyperimmune serum-reactive antigens
PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.
XX
XX Example 7; Page 186; 252pp; English.
XX
XX The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens are
CC used in a vaccine, comprises providing antibody preparation from a plasma
CC pool of a type of animal, or individual sera with antibodies against the
CC specific pathogen, tumour, allergen, tissue or host prone to auto-
CC immunity. The hyperimmune serum-reactive antigens comprising any of the
CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX
XX Sequence 277 AA;
XX
XX Query Match 97.0%; Score 1412; DB 6; Length 277;
XX Best Local Similarity 98.2%; Pred. No. 6.9e-133;
XX Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
XX
XX 1 MAIKKYPITNGRNNTSLDPAITTKTPKSLKLPKAGRNNOGKLTVRHHGGHKKR 60
XX 1 MAIKKYPITNGRNNTSLDPAITTKTPKSLKLPKAGRNNOGKLTVRHHGGHKKR 60
XX
XX 61 QYRVDFPKRNDGINKAKVDSIQVDNRSANIALVWYADGKRTYHCTAPKGLVGGQIVES 120
XX 61 QYRVDFPKRNDGINKAKVDSIQVDNRSANIALVWYADGKRTYHCTAPKGLVGGQIVES 118
XX
XX 121 GAEADTKVGNALPLQIPVGTVVVHNIELPKGKGQIARSAGASQVLGKGGKVLIRLS 180
XX 119 GAEADIKVGNALPLQIPVGTVVVHNIELPKGKGQIARSAGASQVLGKGGKVLIRLS 178
XX
XX 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRSRWKGIPTVRGSMVNPNDPHGGGGR 240
XX 179 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRSRWKGIPTVRGSMVNPNDPHGGGGR 238

QY 241 APIGRSPSPMGKPTLGKTRRGKSSDKLIVRGKKK 279
DB 239 APIGRSPSPMGKPTLGKTRRGKSSDKLIVRGKKK 277
RESULT 6
ABU15836
ID ABU15836 standard; protein; 277 AA.
XX
XX ABU15836;
XX
XX 19-JUN-2003 (first entry)
XX
XX Protein encoded by Prokaryotic essential gene #1363.
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX Staphylococcus aureus.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX
XX 06-SEP-2001; 2001US-00948993.
XX
XX 25-OCT-2001; 2001US-0342923P.
XX
XX 08-FEB-2002; 2002US-00072851.
XX
XX 06-MAR-2002; 2002US-0362899P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
XX
XX N-PSDB; ACA19706.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 43760; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

PT antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 12767; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 277 AA;

Query Match 97.0%; Score 1412; DB 4; Length 277;

Best Local Similarity 98.2%; Pred. No. 6.9e-133;

Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAIKKYKPIITNGRRNMTSLDFAEITKTPKSLKPLPKKAGRNQKLTVRHHGGGHR 60

Db 1 MAIKKYKPIITNGRRNMTSLDFAEITKTPKSLKPLPKKAGRNQKLTVRHHGGGHR 60

QY 61 QYRVDFPKRNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCTAPKGLVGVQIVES 120

Db 61 QYRVDFPKRNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCTAPKGLVGVQIVES 118

QY 121 GAADATKVGNALPLQNI PVGT VVHNI ELKPKGQIARSAGASQV LGKGVYLIRLS 180

Db 119 GAADATKVGNALPLQNI PVGT VVHNI ELKPKGQIARSAGASQV LGKGVYLIRLS 178

QY 181 GEVRMILSTCRATIGQVGNLQHEL VNVYKAGSRWKGI RPTVRGSMVNPNDHPHGGEGR 240

Db 179 GEVRMILSTCRATIGQVGNLQHEL VNVYKAGSRWKGI RPTVRGSMVNPNDHPHGGEGR 238

QY 241 APIGRSPSPWGKPTLGKTRGKSSDKLIVRGRKK 279

Db 239 APIGRSPSPWGKPTLGKTRGKSSDKLIVRGRKK 277

RESULT 4

AAU34212

ID AAU34212 standard; protein; 277 AA.

XX AC AAU34212;

XX DT 14-FEB-2002 (first entry)

XX DE Staphylococcus aureus cellular proliferation protein #488.

XX KW Antisense; prokaryotic cellular proliferation protein; antibiotic;

XX KW antibacterial; drug design.

XX OS Staphylococcus aureus.

XX PN WO200170955-A2.

XX PD 27-SEP-2001.

XX XX 21-MAR-2001; 2001WO-US009180.

XX XX 21-MAR-2000; 2000US-0191078P.

XX XX 23-MAY-2000; 2000US-0206848P.

PR 26-MAY-2000; 2000US-0207727P.

PR 23-OCT-2000; 2000US-0242578P.

PR 27-NOV-2000; 2000US-0253625P.

PR 22-DEC-2000; 2000US-0257931P.

PR 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlson KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

DR N-PSDE; AAS52071.

XX New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 5708; 511pp; English.

PS The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the genes,

CC their use in the discovery of novel antibiotics, the essential genes,

CC themselves and the encoded proteins. The prokaryotes used are Escherichia

CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,

CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also

CC useful for the identification of potential new targets for antibiotic

CC development. The antisense nucleic acids can also be used to identify

CC proteins used in proliferation, to express these proteins, and to obtain

CC antibodies capable of binding to the expressed proteins. The proteins can

CC be used to screen compounds in rational drug discovery programmes. The

CC antisense nucleic acid sequence is also useful to screen for homologous

CC nucleic acids which are required for cell proliferation in a wide variety

CC of organisms. The present sequence represents an essential prokaryotic

CC cellular proliferation protein. Note: The sequence data for this patent

CC did not form part of the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 277 AA;

Query Match 97.0%; Score 1412; DB 4; Length 277;

Best Local Similarity 98.2%; Pred. No. 6.9e-133;

Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAIKKYKPIITNGRRNMTSLDFAEITKTPKSLKPLPKKAGRNQKLTVRHHGGGHR 60

Db 1 MAIKKYKPIITNGRRNMTSLDFAEITKTPKSLKPLPKKAGRNQKLTVRHHGGGHR 60

QY 61 QYRVDFPKRNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCTAPKGLVGVQIVES 120

Db 61 QYRVDFPKRNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCTAPKGLVGVQIVES 118

QY 121 GAADATKVGNALPLQNI PVGT VVHNI ELKPKGQIARSAGASQV LGKGVYLIRLS 180

Db 119 GAADATKVGNALPLQNI PVGT VVHNI ELKPKGQIARSAGASQV LGKGVYLIRLS 178

QY 181 GEVRMILSTCRATIGQVGNLQHEL VNVYKAGSRWKGI RPTVRGSMVNPNDHPHGGEGR 240

Db 179 GEVRMILSTCRATIGQVGNLQHEL VNVYKAGSRWKGI RPTVRGSMVNPNDHPHGGEGR 238

QY 241 APIGRSPSPWGKPTLGKTRGKSSDKLIVRGRKK 279

Db 239 APIGRSPSPWGKPTLGKTRGKSSDKLIVRGRKK 277

RESULT 5

ABJ19004

ID ABJ19004 standard; protein; 277 AA.

XX AC ABJ19004;

XX DT 06-MAR-2003 (first entry)

Db 1 MAIKYKPTITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
QY 61 QYRVDFKRNKOGINAKVDSIQYDPNRSANIALVVTADGEKRIYHCIAPKGLEVGQIVS 120
Db 61 QYRVDFKRNKOGINAKVDSIQYDPNRSANIALVVTADGEKRIYHCIAPKGLEVGQIVS 118
QY 121 GAEADTKVGNALPLQNPVGTVVHNIELKPGKGQIARSAGASAQVLGKGGKYLRLRS 180
Db 119 GAEADTKVGNALPLQNPVGTVVHNIELKPGKGQIARSAGASAQVLGKGGKYLRLRS 178
QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGKRSRWKGIPTVRGSMVNPNDHPHGGGEGR 240
Db 179 GEVRMILSTCRATIGQVGNLQHELNVNKGKRSRWKGIPTVRGSMVNPNDHPHGGGEGR 238
QY 241 APIGRSPSPMGKPTLGKTRRGKSSDKLIVRGKKK 279
Db 239 APIGRSPSPMGKPTLGKTRRGKSSDKLIVRGKKK 277

RESULT 2

AAU36656
ID AAU36656 standard; protein; 277 AA.

XX AC AAU36656;
XX DT

XX 14-FEB-2002 (first entry)

XX Staphylococcus aureus cellular proliferation protein #826.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;

XX Antibacterial; drug design.

XX Staphylococcus aureus.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

XX 26-MAY-2000; 2000US-0207727P.

XX 23-OCT-2000; 2000US-0242578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257931P.

XX 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

XX Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

XX N-PSDB; AAS54515.

XX New polynucleotides for the identification and development of

XX antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 12249; 51pp; English.

XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the genes,
XX their use in the discovery of novel antibiotics, the essential genes
XX themselves and the encoded proteins. The prokaryotes used are Escherichia
XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX useful for the identification of potential new targets for antibiotic
XX development. The antisense nucleic acids can also be used to identify
XX proteins used in proliferation, to express these proteins, and to obtain
XX antibodies capable of binding to the expressed proteins. The proteins can
XX be used to screen compounds in rational drug discovery programmes. The

CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 277 AA;

Query Match 97.0%; Score 1412; DB 4; Length 277;

Best Local Similarity 98.2%; Pred. No. 6.9e-133;

Matches 2/4; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAIKYKPTITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60

Db 1 MAIKYKPTITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60

QY 61 QYRVDFKRNKOGINAKVDSIQYDPNRSANIALVVTADGEKRIYHCIAPKGLEVGQIVS 120

Db 61 QYRVDFKRNKOGINAKVDSIQYDPNRSANIALVVTADGEKRIYHCIAPKGLEVGQIVS 118

QY 121 GAEADTKVGNALPLQNPVGTVVHNIELKPGKGQIARSAGASAQVLGKGGKYLRLRS 180

Db 119 GAEADTKVGNALPLQNPVGTVVHNIELKPGKGQIARSAGASAQVLGKGGKYLRLRS 178

QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGKRSRWKGIPTVRGSMVNPNDHPHGGGEGR 240

Db 179 GEVRMILSTCRATIGQVGNLQHELNVNKGKRSRWKGIPTVRGSMVNPNDHPHGGGEGR 238

QY 241 APIGRSPSPMGKPTLGKTRRGKSSDKLIVRGKKK 279

Db 239 APIGRSPSPMGKPTLGKTRRGKSSDKLIVRGKKK 277

RESULT 3

AAU37174

ID AAU37174 standard; protein; 277 AA.

XX AC AAU37174;

XX 14-FEB-2002 (first entry)

XX Staphylococcus aureus cellular proliferation protein #1344.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;

XX Antibacterial; drug design.

XX Staphylococcus aureus.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

XX 26-MAY-2000; 2000US-0207727P.

XX 23-OCT-2000; 2000US-0242578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257931P.

XX 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

XX Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

XX N-PSDB; AAS55033.

XX New polynucleotides for the identification and development of

XX PT

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OM protein - protein search, using sw model

Run on: June 9, 2005, 15:48:59 ; Search time 161 Seconds
(without alignments)
670.225 Million cell updates/sec

Title: US-09-839-695B-13

Perfect score: 1456

Sequence: 1 MAIKKYKPIITNGRRNMTSLD.....KTRRGKSSDKLIVRGKKK 279

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1412	97.0	277	3	AAY70416 Staphyloc
2	1412	97.0	277	4	Aau36656 Staphyloc
3	1412	97.0	277	4	Aau37174 Staphyloc
4	1412	97.0	277	4	Aau34212 Staphyloc
5	1412	97.0	277	6	Abj19004 Pathogen
6	1412	97.0	277	6	Abu15836 Protein e
7	1412	97.0	277	6	Abm72939 Staphyloc
8	1380	94.8	277	6	Abu43554 Protein e
9	1375	94.4	279	5	Abp38415 Staphyloc
10	1375	94.4	279	8	Adso7076 Staphyloc
11	1373	94.3	277	6	Abj19022 Pathogen
12	1373	94.3	277	6	Abu42626 Protein e
13	1203	82.6	277	5	Abb49366 Listeria
14	1203	82.6	277	6	Abu32542 Protein e
15	1163	79.9	277	8	Adsa4623 Bacterial
16	1154	79.3	276	8	Adso7071 Bacterial
17	1121	77.0	277	6	Abu46394 Protein e
18	1120	76.9	276	4	Aau34962 Enterococ
19	1120	76.9	276	6	Abu14500 Protein e
20	1117	76.7	277	5	Abp28608 Streptoco
21	1112	76.4	274	4	Aau33423 Enterococ
22	1108	76.1	277	4	Aau37607 Streptoco
23	1108	76.1	277	4	Aau37946 Streptoco
24	1108	76.1	277	6	Abu00552 S. pneumo
25	1108	76.1	277	6	Abp81521 Streptoco

ALIGNMENTS

RESULT 1

AAY70416

ID AAY70416 standard; protein; 277 AA.

XX AAY70416;

XX 21-JUN-2000 (first entry)

XX Staphylococcus aureus ribosomal protein RPL2.

XX S10-spc ribosomal operon; ribosomal protein; RPL2; screening; diagnosis;
KW antibacterial agent; treatment; prevention; bacterial infection.

XX Staphylococcus aureus.

XX WO200011184-A1.

XX 02-MAR-2000.

XX 23-AUG-1999; 99WO-US019298.

XX 25-AUG-1998; 98US-00139234.

XX (SCHE) SCHERING CORP.

XX Shimer GH, Hare RS, Shaw KJ, Black T;

XX WPI; 2000-256379/22.

XX N-PSDB; AAZ51566.

XX New Staphylococcus aureus polypeptides used for isolating antibacterial agent for treating bacterial infections.

XX Claim 1; Page 28-29; 42pp; English.

XX The present sequence is a ribosomal protein RPL2 from S10-spc operon of Staphylococcus aureus ATCC 55748. The protein is used as a target for screening broad spectrum antibacterial agents which can be used to prevent or treat diseases caused by bacteria. This sequence is also useful in the diagnosis of bacterial infections

XX Sequence 277 AA;

Query Match 97.0% Score 1412; DB 3; Length 277;

Best Local Similarity 98.2%; Pred. No. 6.9e-133;

Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAIKKYKPIITNGRRNMTSLDFABITTPEKSLKLPKKGRRNNQGLTVRRHGGGHR 60

A:Molecule type: DNA
A:Residues: 1-6,'N',8-18,'TECSLFNNOKIA','31-35,'GG','38-41,'TA','44-46,'KS','49-51,'SS','54-58-
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: ribosomal protein L2/L8
C:Keywords: protein biosynthesis, ribosome

Query Match 65.8%; Score 958; DB 1; Length 281;
Best Local Similarity 65.0%; Pred.No. 2.2e-68;
Matches 184; Conservative 40; Mismatches 53; Indels 6; Gaps 3;

Qy 1 MAIKKYPITNGRRNMISLDFAEI--TKTTPKSLLLPLPKKAGRNNOGKLTVRHGGGH 58
 |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db 1 MAIKKYKSTNGRRNMITIDYSAVLTTKTNPESLSVSKSGGRNRGLITTRHKGGGH 60

Qy 59 KQRYRVDDFKENKGGINAKVDISIQDPPRSANIALVVYADGEKRIYHCCTAPKGLEVGQIV 118
 ||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db 61 KQRYIIIDFKENKRDIIFGTISTIEDPNRNAFICLVNYVDYEKR--YILFAKMGMVMKV 118

Qy 119 ESGAEADTKGNALPLONI PVGTVVHNTELKPCKGOIARSASAOVLGK--EGKYVLI 176
 ::::::::::::||:::||:::||:::||:::||:::||:::||:::||:::||
Db 119 VASENADIKGNAPLPKNIPGTLHNLVELPKCGOIRARSAGSVQLLGKDDRGYYVL 178

Qy 177 RLRSSEVRMILSTCRATIGQVGNLQHELVNVYGKGRSWKGI RPTVRGSVMNPNDHPHG 236
 |||||:::||:::||:::||:::||:::||:::||:::||:::||
Db 179 RLSSGEVRKVLSECYATIGEVEENEYINLVWGKAGRNRWGI RPTVRGSVMNPNDQPHG 238

Qy 237 GEGRAPTGRPSPMSPGWKPTLGKKTRRKKSDKLI VRKKK 279

Db 239 GEGRAPTGRKSPVTMPWKALGVKTRNTKKASEKLIVRKSKK 281

RESULT 13
 A99585
 50S ribosomal protein L2 [imported] - Mycoplasma pulmonis (strain UAB CTTP)
 C;Species: Mycoplasma pulmonis
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C;Accession: A99585
 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissou, F.; Moszer, I.;
 Nucleic Acids Res. 29, 2145-2153, 2001
 A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
 A;Reference number: A99512; MUID:21267165; PMID:11353084
 A;Accession: A99585
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-281 <KUR>
 A;Cross-references: UNIPROT:Q98PY4; GB:AL445566; PID:g14090000; PIDN:CAC13758.1; GSPDB:GN
 A;Experimental source: strain UAB CTTP
 C;Genetics:
 A;Gene: MYPU 5850
 A;Genetic code: SGC3
 C;Superfamily: ribosomal protein L2/L8

	Matches	181,	Conservative	37,	Mismatches	58,	Indels	5,	Gaps	3;
Qy	1	MAIKKYPI	TNGRRNMTSLDF	-	AEIKTKTTP	PKSLKPLPKK	AGRNNOGKLT	VRHHGGG	HK	59
Db	1	MAIRKL	PTNGTNRMSLTD	YKTNLTG	HAPBSKLMKIL	LKNSGRNR	GVITTRHGG	GREK		60
Qy	60	ROYRVID	FKRNKDGINAKVDS	IGQDPNRS	ANIALV	VYADG	EKKRIYHCIA	PKGLEVG	QIVE	119
Db	61	RFYRLVDF	FKRNKDNI	EAIKTKT	IEYDPNRS	ANISL	VTYLDG	EKKR--	YILSPKGI	KVGQRIV 118
Qy	120	SGEADT	KVGNALPLQNI	PGVTGVH	NIELK	CKGGOI	ARSAGAS	AQVLKE--	GKVVLIR	177
Db	119	SGENV	DIIVGNSLE	LANIPEGTN	IHNIELQ	FKGGGIL	ARSAGSYAQIL	CKESGK	VLIR	178
Qy	178	LRSGE	VRMI	ISTCR	ATIGQVGN	LQHELNV	VGKAGSR	RWKGI	PTVRGS	VYMNPDHPHGGG 237
Db	179	LKSGE	VRKVF	AKCR	ATIGVNE	BEHSLVNI	GKAGRN	RHKGI	PTVRGS	VYMNIDHPHGGG 238

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Db 1 MGIRVYKPTTNGRRNMTSLDFAEITTTPEKSLLVALKSAGRNNGRIITVRHGGGHR 60
QY 61 QYRVIDPKRKGGINAKVDSIQYDPPNRANIALVYVADGKRIYHCIAPKGLEVGQIVS 120
Db 61 FYRLVDFPKRKNQVAVVKTIEYDPPNRANIALVHYTDGVKA--YIIAPKGLEVGQRIVS 118
QY 121 GAADTKVGNALPLQNIPIVGTVVVHNIELKPGKGQIARSAGASAOVLGKEGKTVLRLRS 180
Db 119 GPEADIKVGNALPLANIPVGTTLHNIELKPGRGELVRAAGASAOVLGSEKTVLRLQS 178
QY 181 GEVRMILSTCRATIGOVNLOHVLNVGKAGRWKGIPTVRGSMVNPNDHPHGGEGR 240
Db 179 GEVRMILGTCTATVGVVGVNEQHLVNLGKAGRWKGIPTVRGSMVNPNDHPHGGEGR 238
QY 241 APICRPSMPGKPTLGKTRGKSSDKLIIVRGRKK 279
Db 239 APVGRKAPSTPWGKPALGLTRNKKAKSDKLIIVRRNEK 277

RESULT 8
G97895
50S ribosomal protein L2 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: G97895
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; H
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: G97895
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <KUR>
A;Cross-references: UNIPROT:Q97SV2; UNIPROT:Q8CWV5; GB:AE007317; PIDN:AAK98995.1; PID:g1
C;Genetics:
A;Gene: rplB
A;Superfamily: ribosomal protein L2/L8

Query Match 76.1%; Score 1108; DB 2; Length 277;
Best Local Similarity 75.3%; Pred. No. 3e-80;
Matches 210; Conservative 26; Mismatches 41; Indels 2; Gaps 1;

QY 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLLVALKSAGRNNGRIITVRHGGGHR 60
Db 1 MGIRVYKPTTNGRRNMTSLDFAEITTTPEKSLLVALKSAGRNNGRIITVRHGGGHR 60
QY 61 QYRVIDPKRKGGINAKVDSIQYDPPNRANIALVYVADGKRIYHCIAPKGLEVGQIVS 120
Db 61 FYRLVDFPKRKNQVAVVKTIEYDPPNRANIALVHYTDGVKA--YIIAPKGLEVGQRIVS 118
QY 121 GAADTKVGNALPLQNIPIVGTVVVHNIELKPGKGQIARSAGASAOVLGKEGKTVLRLRS 180
Db 119 GPEADIKVGNALPLANIPVGTTLHNIELKPGRGELVRAAGASAOVLGSEKTVLRLQS 178
QY 181 GEVRMILSTCRATIGOVNLOHVLNVGKAGRWKGIPTVRGSMVNPNDHPHGGEGR 240
Db 179 GEVRMILGTCTATVGVVGVNEQHLVNLGKAGRWKGIPTVRGSMVNPNDHPHGGEGR 238
QY 241 APICRPSMPGKPTLGKTRGKSSDKLIIVRGRKK 279
Db 239 APVGRKAPSTPWGKPALGLTRNKKAKSDKLIIVRRNEK 277

RESULT 9
H86886
50S ribosomal protein L2 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86886
```

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R;Bolotin, A.; Wincker, P.; Mauer, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlic
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86886
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <STO>
A;Cross-references: UNIPROT:Q9CDW5; GB:AE005176; PID:g12725150; PIDN:AAK06194.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: rplB
C;Superfamily: ribosomal protein L2/L8

Query Match 73.6%; Score 1072; DB 2; Length 276;
Best Local Similarity 74.8%; Pred. No. 2.1e-77;
Matches 205; Conservative 24; Mismatches 43; Indels 2; Gaps 1;

QY 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLLVALKSAGRNNGRIITVRHGGGHR 60
Db 1 MGIRVYKPTTNGRRNMTSGDFAEITTTPEKSLLVSMKTAGRNNTGRITVRHGGGHR 60
QY 61 QYRVIDPKRKGGINAKVDSIQYDPPNRANIALVYVADGKRIYHCIAPKGLEVGQIVS 120
Db 61 KYRVIDFKRTTNDVAKVAIIEDPNTANIALIVISGVKS--YIIAPKGLEVGTVVS 118
QY 121 GAADTKVGNALPLQNIPIVGTVVVHNIELKPGKGQIARSAGASAOVLGKEGKTVLRLRS 180
Db 119 GPEADIKVGNALPLANIPVGTTLHNIELKPGGQLVRSAGASAOVLGSEKTVLRLQS 178
QY 181 GEVRMILSTCRATIGOVNLOHVLNVGKAGRWKGIPTVRGSMVNPNDHPHGGEGR 240
Db 179 GEVRMILSTCRATIGVGVNEQSLNLGKAGTRHMGIRPTVRGSMVNPNDHPHGGEGR 238
QY 241 APICRPSMPGKPTLGKTRGKSSDKLIIVR 274
Db 239 QVGRKSPMPGKPALGLTRNKKAKSKLIIVR 272

RESULT 10
B54547
ribosomal protein l2 - mycoplasma-like organism MLO
C;Species: mycoplasma-like organisms, MLOs
C;Date: 06-Oct-1994 #sequence_revision 25-Apr-1997 #text_change 07-Jul-2003
C;Accession: B54547
R;Lim, P.O.; Sears, B.B.
FEMS Microbiol. Lett. 68, 71-73, 1991
A;Title: DNA sequence of the ribosomal protein genes rpl2 and rps19 from a plant-pathogen
A;Reference number: A54547; MUID:92120503; PMID:1769558
A;Accession: B54547
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <LIM>
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBI:77580, NCBI:77582)
C;Superfamily: ribosomal protein L2/L8

Query Match 66.7%; Score 971; DB 2; Length 276;
Best Local Similarity 68.0%; Pred. No. 2e-69;
Matches 189; Conservative 30; Mismatches 57; Indels 2; Gaps 1;

QY 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLLVALKSAGRNNGRIITVRHGGGHR 60
Db 1 MAIKKYKPTTNGRRNMTSVSAFSEITTTQTPKRLVSHKDAQAGRNNGKITVRHGGGHR 60
QY 61 QYRVIDPKRKGGINAKVDSIQYDPPNRANIALVYVADGKRIYHCIAPKGLEVGQIVS 120
Db 61 KYRVIDFKRKNQIVGVKATIEYDPPNRANIALHYLDGEK--YIIAPKGLTVGMQIVS 118
QY 121 GAADTKVGNALPLQNIPIVGTVVVHNIELKPGKGQIARSAGASAOVLGKEGKTVLRLRS 180
Db 119 GKEADIKVANCILSLMNIPIVGTVVVHNIELKPGKGQIARSASQFCQIISREDKTVLRLQS 178
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C;Accession: AE1403
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative Genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
C;Accession: AE1403
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <GLA>
A;Cross-references: UNIPROT:P60426; GB:NC_003210; PIDN:CAD00707.1; PID:g16412117; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: rplB
C;Superfamily: ribosomal protein L2/L8

Query Match 82.6%; Score 1203; DB 2; Length 277;
Best Local Similarity 82.4%; Pred. No. 9.1e-88;
Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;

QY 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLRLPLKKKAGRNNOGKLTVRHHGGGHR 60
DB 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLRLPLKKKAGRNNOGKLTVRHHGGGHR 60

QY 61 QYRVDFKRNKDGKINAKVDSIQYDPNRSANIALVVTADGKRIYHCITAPKGLVGOIVES 120
DB 61 QYRVDFKRNKDGKINAKVDSIQYDPNRSANIALVVTADGKRIYHCITAPKGLVGOIVES 118

QY 121 GAEADTKVGNALPLQNIPIVGTVVHNIELKPGKGQIARSAGASAOVLGKGGKVLRLRS 180
DB 119 GAEADTKVGNALPLQNIPIVGTVVHNIELKPGKGQIARSAGASAOVLGKGGKVLRLRS 178

QY 181 GEVRMILSTCRATIGQVGNLQHLVNVGKAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVRMILSTCRATIGQVGNLQHLVNVGKAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 238

QY 241 APIGRSPSPMGKPTLGKTRGKSSDKLIVRGKKK 279
DB 239 APIGRSPSPMGKPTLGKTRKNNNSDKFIVRRKKK 277

RESULT 3
AD1779
ribosomal protein L2 [imported] - *Listeria innocua* (strain Clp11262)
C;Species: *Listeria innocua*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1779
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative Genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
C;Accession: AD1779
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <GLA>
A;Cross-references: UNIPROT:P60425; GB:AL592022; PIDN:CAC98004.1; PID:g16415314; GSPDB:
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: rplB
C;Superfamily: ribosomal protein L2/L8

Query Match 82.6%; Score 1203; DB 2; Length 277;
Best Local Similarity 82.4%; Pred. No. 9.1e-88;
Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;

QY 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLRLPLKKKAGRNNOGKLTVRHHGGGHR 60

DB 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLRLPLKKKAGRNNOGKLTVRHHGGGHR 60
QY 61 QYRVDFKRNKDGKINAKVDSIQYDPNRSANIALVVTADGKRIYHCITAPKGLVGOIVES 120
DB 61 QYRVDFKRNKDGKINAKVDSIQYDPNRSANIALVVTADGKRIYHCITAPKGLVGOIVES 118

QY 121 GAEADTKVGNALPLQNIPIVGTVVHNIELKPGKGQIARSAGASAOVLGKGGKVLRLRS 180
DB 119 GAEADTKVGNALPLQNIPIVGTVVHNIELKPGKGQIARSAGASAOVLGKGGKVLRLRS 178

QY 181 GEVRMILSTCRATIGQVGNLQHLVNVGKAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVRMILSTCRATIGQVGNLQHLVNVGKAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 238

QY 241 APIGRSPSPMGKPTLGKTRGKSSDKLIVRGKKK 279
DB 239 APIGRSPSPMGKPTLGKTRKNNNSDKFIVRRKKK 277

RESULT 4
F69694
ribosomal protein L2 (BL2) rplB - *Bacillus subtilis*
C;Species: *Bacillus subtilis*
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F69694
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc, iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Segiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Torato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: F69694
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-277 <KUN>
A;Cross-references: UNIPROT:P42919; GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11895.1
A;Experimental source: strain 168
C;Genetics:
A;Gene: rplB
C;Superfamily: ribosomal protein L2/L8

Query Match 79.9%; Score 1163; DB 2; Length 277;
Best Local Similarity 79.9%; Pred. No. 1.3e-84;
Matches 223; Conservative 19; Mismatches 35; Indels 2; Gaps 1;

QY 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLRLPLKKKAGRNNOGKLTVRHHGGGHR 60
DB 1 MAIKKYKPSNGRRGNTTSDFAEITTTPEKSLRLPLKKKAGRNNOGKLTVRHHGGGHR 60

QY 61 QYRVDFKRNKDGKINAKVDSIQYDPNRSANIALVVTADGKRIYHCITAPKGLVGOIVES 120
DB 61 QYRVDFKRNKDGKINAKVDSIQYDPNRSANIALVVTADGKRIYHCITAPKGLVGOIVES 118

QY 121 GAEADTKVGNALPLQNIPIVGTVVHNIELKPGKGQIARSAGASAOVLGKGGKVLRLRS 180
DB 119 GAEADTKVGNALPLQNIPIVGTVVHNIELKPGKGQIARSAGASAOVLGKGGKVLRLRS 178

QY 181 GEVRMILSTCRATIGQVGNLQHLVNVGKAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVRMILSTCRATIGQVGNLQHLVNVGKAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 238

QY 241 APIGRSPSPMGKPTLGKTRGKSSDKLIVRGKKK 279

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 9, 2005, 15:57:59 ; Search time 40 Seconds
(without alignments)
671.112 Million cell updates/sec

Title: US-09-839-695B-13
Perfect score: 1456
Sequence: 1 MAIKKYKPIITNGRRNMTSLD.....KTRRGKSSDKLIVRGRKKK 279

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1412	97.0	277	B90022	50S ribosomal prot
2	1203	82.6	277	AD1403	ribosomal protein
3	1203	82.6	277	AD1779	ribosomal protein
4	1163	79.9	277	F69694	ribosomal protein
5	1154	79.3	276	T44386	ribosomal protein
6	1125	77.3	275	R5B2F	ribosomal protein
7	1108	76.1	277	G95024	ribosomal protein
8	1108	76.1	277	G97895	50S ribosomal prot
9	1072	73.6	276	H86886	50S ribosomal prot
10	971	66.7	276	B54547	ribosomal protein
11	969	66.6	277	B97285	ribosomal protein
12	958	65.8	281	R5YM2C	ribosomal protein
13	920.5	63.2	281	A99585	50S ribosomal prot
14	897	61.6	287	AE2332	50S ribosomal prot
15	895	61.5	279	C82915	ribosomal protein
16	885	60.8	275	B75534	ribosomal protein
17	880	60.4	280	C70642	probable ribosomal
18	876	60.2	274	C82059	ribosomal protein
19	871.5	59.9	276	A72550	ribosomal protein
20	862.5	59.2	274	R5EBY	ribosomal protein
21	862.5	59.2	274	AE0026	50S ribosomal prot
22	855	58.7	275	R5KT2	ribosomal protein
23	855	58.7	280	T45367	ribosomal protein
24	846	58.1	275	S78273	ribosomal protein
25	843	57.9	277	D82005	50S ribosomal prot
26	842	57.8	276	S77499	ribosomal protein
27	842	57.8	277	C81231	50S ribosomal prot
28	838	57.6	273	B83116	50S ribosomal prot
29	837.5	57.5	273	R5EC2	ribosomal protein

30	837.5	57.5	273	2	B85997	50S ribosomal subu
31	837.5	57.5	273	2	F91151	50S ribosomal subu
32	836.5	57.5	273	2	AD1006	50S ribosomal chai
33	834.5	57.3	273	2	H64092	ribosomal protein
34	823.5	56.6	273	2	F84990	50S ribosomal prot
35	819.5	56.3	276	2	D81268	50S ribosomal prot
36	816	56.0	277	2	S26081	ribosomal protein
37	813.5	55.9	277	2	H70159	ribosomal protein
38	812.5	55.8	275	2	C82717	50S ribosomal prot
39	810.5	55.7	294	2	S73232	ribosomal protein
40	806	55.4	275	2	T07361	ribosomal protein
41	806	55.4	285	2	A64217	ribosomal protein
42	786	54.0	277	1	R5LV2	ribosomal protein
43	782	53.7	273	2	B71355	probable ribosomal
44	781	53.6	287	2	S73989	ribosomal protein
45	774	53.2	277	2	AB3347	LSU ribosomal prot

ALIGNMENTS

RESULT 1

B90022
50S ribosomal protein L2 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B90022
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; f
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: B90022
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <KUR>
A;Cross-references: UNIPROT:P60432; GB:BA000018; PID:g13702047; PIDN:BA843339.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: rplB
C;Superfamily: ribosomal protein L2/L8

Query Match	97.0%	Score 1412;	DB 2;	Length 277;
Best Local Similarity	98.2%;	Pred. No. 2.7e-104;		
Matches 274;	Conservative 1;	Mismatches 2;	Indels 2;	Gaps 1;
Qy	1	MAIKKYKPIITNGRRNMTSLDFAEITKTPPEKSLKPLPKKAGRNNOGKLTVRHHGGGHR	60	
Db	1	MAIKKYKPIITNGRRNMTSLDFAEITKTPPEKSLKPLPKKAGRNNOGKLTVRHHGGGHR	60	
Qy	61	QYRVDFPKRNKGINAKVDSIQYDNPNSANIALVYVADGKKRIYHCITAPKGLEVGQIVES	120	
Db	61	QYRVDFPKRNKGINAKVDSIQYDNPNSANIALVYVADGKKR--YITAPKGLEVGQIVES	118	
Qy	121	GAEADTKVGNALPLQNIIPVGTVVHNIETLKPQGGQIARSAGASAOVLGKEGKYVLIRLS	180	
Db	119	GAEADIKVGNALPLQNIIPVGTVVHNIETLKPQGGQIARSAGASAOVLGKEGKYVLIRLS	178	
Qy	181	GEVRMILSTCRATIGQVGNLQHELNVNNGKAGRSRWKGIPTVRGSMVNPNDHPHGGEGR	240	
Db	179	GEVRMILSTCRATIGQVGNLQHELNVNNGKAGRSRWKGIPTVRGSMVNPNDHPHGGEGR	238	
Qy	241	APIGRSPSPMGKPTLGKTKTRGKSSDKLIVRGRKKK	279	
Db	239	APIGRSPSPMGKPTLGKTKTRGKSSDKLIVRGRKKK	277	

RESULT 2

AE1403
ribosomal protein L2 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

Search completed: June 9, 2005, 16:07:21
Job time : 176 secs

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DR EMBL; AP001507; BAB03856.1; -.
DR PIR; T44386; T44386.
DR HSP; P04257; 1RL2.
DR HAMAP; MF_01320; -. 1.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR002171; Ribosomal_L2.
DR InterPro; IPR005880; Ribosomal_L2_b/o.
DR InterPro; IPR008991; Transl_SH3_like.
DR Pfam; PF00181; Ribosomal_L2; 1.
DR Pfam; PF03947; Ribosomal_L2_C; 1.
DR TIGRFAMs; TIGR01171; rplB_bact; 1.
DR PROSITE; PS00467; RIBOSOMAL_L2; 1.
KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.
SQ SEQUENCE 276 AA; 30224 MW; ABD31A20D6479696 CRC64;

Query Match          79.3%; Score 1154; DB 1; Length 276;
Best Local Similarity 78.4%; Pred. No. 2.9e-8;
Matches 218; Conservative 23; Mismatches 35; Indels 2; Gaps 1;

QY 1 MAIKKYKPTNGRRNMTSLDFAETTKTTPKSLKLPKPKAGRNQCKLTVRHGGGCHKR 60
DB 1 MAIKKYKPTNGRRNMTSLDFAETTKTTPKSLKLPKPKAGRNQCKLTVRHGGGCHKR 60

QY 61 QYRVDFPKRNDGINAKVDSIQYDPRNSANTALVYVYADGKRIYHCIAPKGLEVGQIVES 120
DB 61 QYRIIDFKRNDGIPGRVATIEYDPRNSANTALINYVDGKR--YILAPKGLKVGMTIES 118

QY 121 GAEDATKVGNALPLQNIPTVGTVVHNIELKPKGQIARSAGASAOVLGKGGKYLIRLS 180
DB 121 GAEDATKVGNALPLQNIPTVGTVVHNIELKPKGQIARSAGASAOVLGKGGKYLIRLS 180

QY 119 GAEDATKVGNALPLQNIPTVGTVVHNIELKPKGQIARSAGASAOVLGKGGKYLIRLS 178
DB 119 GAEDATKVGNALPLQNIPTVGTVVHNIELKPKGQIARSAGASAOVLGKGGKYLIRLS 178

QY 181 GEVRMILSTCRATIGQVGNLOHLELVNKGAGRSWKGIPTVRGVSVMNPDHPHGGGEGR 240
DB 181 GEVRMILSTCRATIGQVGNLOHLELVNKGAGRSWKGIPTVRGVSVMNPDHPHGGGEGR 240

QY 179 GEVRLVLSACRATVGVGNESHELKIKGAGRSWLKRPPTVRGVSVMNPDHPHGGGEGR 238
DB 179 GEVRLVLSACRATVGVGNESHELKIKGAGRSWLKRPPTVRGVSVMNPDHPHGGGEGR 238

QY 241 APIGRSPSPMGKPTLGKTRGKSSDKLIVRGRKK 278
DB 241 APIGRSPSPMGKPTLGKTRGKSSDKLIVRGRKK 278

QY 239 SPIGRKSPSPMGKPTLGKTRKKNKASDKFIVRRKK 276
DB 239 SPIGRKSPSPMGKPTLGKTRKKNKASDKFIVRRKK 276

RESULT 15
RL2_BACAN
ID - RL2_BACAN STANDARD; PRT; 276 AA.
AC O81VS7; O614T1; O6KVH7;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L2.
GN Name=rplB; OrderedLocusNames=BA01113, GBAA01113, BAS01113;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Oksstad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman J.F.,
RA Berry K.J., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Hazen A.L., Clime R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate 0581;

```

```

RA Ravel J., Raeko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RN Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RL [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Stjerne;
RA Brettn T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RA Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: One of the primary rRNA binding proteins. Required for
CC association of the 30S and 50S subunits to form the 70S ribosome,
CC for rRNA binding and peptide bond formation. It has been suggested
CC to have peptidyltransferase activity; this is somewhat
CC controversial. Makes several contacts with the 16S rRNA in the 70S
CC ribosome (By similarity).
CC -1- SUBUNIT: Part of the 70S ribosome (By similarity).
CC -1- SIMILARITY: Belongs to the ribosomal protein L2p family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AE017024; AAT24167.1; -.
CC EMBL; AE017334; AAT29193.1; -.
CC EMBL; AE017225; AAT52450.1; -.
CC HSP; P04257; 1RL2.
CC TIGR; BA01113; -.
CC HAMAP; MF_01320; -. 1.
CC InterPro; IPR008994; Nucleic_acid_OB.
CC InterPro; IPR002171; Ribosomal_L2_
CC InterPro; IPR005880; Ribosomal_L2_b/o.
CC InterPro; IPR008991; Transl_SH3_like.
CC Pfam; PF00181; Ribosomal_L2; 1.
CC Pfam; PF03947; Ribosomal_L2_C; 1.
CC TIGRFAMs; TIGR01171; rplB_bact; 1.
CC PROSITE; PS00467; RIBOSOMAL_L2; 1.
KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.
SQ SEQUENCE 276 AA; 30253 MW; FE3202D9F89FDE90 CRC64;

Query Match          78.2%; Score 1139; DB 1; Length 276;
Best Local Similarity 77.7%; Pred. No. 4.3e-81;
Matches 216; Conservative 22; Mismatches 38; Indels 2; Gaps 1;

QY 1 MAIKKYKPTNGRRNMTSLDFAETTKTTPKSLKLPKPKAGRNQCKLTVRHGGGCHKR 60
DB 1 MGIKKYNPTNGRRNMTTNDFAETTTDRPEKSLIAPLSKAGRNQCKITVRHGGGCHKR 60

QY 61 QYRVDFPKRNDGINAKVDSIQYDPRNSANTALVYVYADGKRIYHCIAPKGLEVGQIVES 120
DB 61 QYRIIDFKRNDGIPGRVATIEYDPRNSANTALINYVDGKR--YILAPKGLKVGMEIMS 118

QY 121 GAEDATKVGNALPLQNIPTVGTVVHNIELKPKGQIARSAGASAOVLGKGGKYLIRLS 180
DB 121 GAEDATKVGNALPLQNIPTVGTVVHNIELKPKGQIARSAGASAOVLGKGGKYLIRLS 180

QY 119 GAEDATKVGNALPLQNIPTVGTVVHNIELKPKGQIARSAGASAOVLGKGGKYLIRLS 178
DB 119 GAEDATKVGNALPLQNIPTVGTVVHNIELKPKGQIARSAGASAOVLGKGGKYLIRLS 178

QY 181 GEVRMILSTCRATIGQVGNLOHLELVNKGAGRSWKGIPTVRGVSVMNPDHPHGGGEGR 240
DB 181 GEVRMILSTCRATIGQVGNLOHLELVNKGAGRSWKGIPTVRGVSVMNPDHPHGGGEGR 240

QY 179 GEVRLVLSACRATVGVGNESHELKIKGAGRSWLKRPPTVRGVSVMNPDHPHGGGEGR 238
DB 179 GEVRLVLSACRATVGVGNESHELKIKGAGRSWLKRPPTVRGVSVMNPDHPHGGGEGR 238

QY 241 APIGRSPSPMGKPTLGKTRGKSSDKLIVRGRKK 278
DB 241 APIGRSPSPMGKPTLGKTRGKSSDKLIVRGRKK 278

QY 239 SPIGRKSPSPMGKPTLGKTRKKNKASDKFIVRRKK 276
DB 239 SPIGRKSPSPMGKPTLGKTRKKNKASDKFIVRRKK 276

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Db 1 AIKKYPSNRRGMTTSDFAEITTTDKPEKSLIAPLHKGGRRNQKGLTVRHQGGGHKQ 60
QY 62 YRVDFKRNKDGINAKVDSIQYDNPNSANIALVYADGEKRIYHCIAPKGLEVGQIVESG 121
Db 61 YRVDFKRDGIGIPGRVATVEYDNPNSANIALVYADGEKRIYHCIAPKGLEVGQIVESG 118
QY 122 AADTKVGNALPLONIPVGTWVHNIELKPKGGQIARSAGASAOVLGKEGKYVLIRLSG 181
Db 119 PEADIKVGNALPLINIPVGTWVHNIELKPKGGQIARSAGASAOVLGKEGKYVLIRLSG 178
QY 182 EVRMILSTCRATIGQVGNLQHELVNKGKRSWKGIPTVRGSGVNNPNDHPHGGGEGRA 241
Db 179 EVRMILSACRASIGQVNEGHELVNKGKRSWKGIPTVRGSGVNNPNDHPHGGGEGRA 238
QY 242 PIGRSPSPMGKPTLGKTKRRGKSSDKLIVRGRKK 279
Db 239 PIGRSPSPMGKPTLFTKTRKQKNSDKFIVRRKKNK 276

RESULT 13
RL2_OCEIH STANDARD; PRT; 276 AA.
AC QBETX9;
DT 28-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L2.
GN Name=rpL2; OrderedLocusNames=OB0122;
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments."
RL Nucleic Acids Res. 30:3927-3935(2002).
CC -!- FUNCTION: One of the primary rRNA binding proteins. Required for
CC association of the 30S and 50S subunits to form the 70S ribosome,
CC for rRNA binding and peptide bond formation. It has been suggested
CC to have peptidyltransferase activity; this is somewhat
CC controversial. Makes several contacts with the 16S rRNA in the 70S
CC ribosome (By similarity).
CC -!- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the
CC 30S subunit in the 70S ribosome (By similarity).
CC -!- SIMILARITY: Belongs to the ribosomal protein L2P family.
CC -----
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CC -----
CC EMBL; AP004593; BAC12078.1; -;
CC HSSP; P04257; IRL2. -;
CC HAWAP; MF_01326; -; 1.
CC InterPro; IPR008994; Nucleic acid OB.
CC InterPro; IPR002171; Ribosomal L2.
CC InterPro; IPR005880; Ribosomal L2 b/o.
CC InterPro; IPR008991; Transl SH3 like.
CC Pfam; PF00181; Ribosomal L2; 1.
CC Pfam; PF03947; Ribosomal L2_C; 1.
CC TIGRFAMs; TIGR01171; rplB_bact; 1.
CC PROSITE; PS00467; RIBOSOMAL L2; 1.
CC Complete proteome; Ribosomal protein; rRNA-binding; rRNA-binding.
CC KW PROSITE; PS00467; RIBOSOMAL L2; 1.
CC SEQUENCE 276 AA; 30386 MW; C9E5E6F0670F9CA0 CRC64;

Query Match 79.4%; Score 1156; DB 1; Length 276;

Best Local Similarity 78.8%; Pred. No. 2e-82;
Matches 219; Conservative 26; Mismatches 31; Indels 2; Gaps 1;
QY 1 MAIKKYKPTNGRNMTSLDFABITTTPEKSLIAPLHKGGRRNQKGLTVRHQGGGHKQ 60
Db 1 MAIKKEKPTNGRNMTSLDFABITTTPEKSLIAPLHKGGRRNQKGLTVRHQGGGHKQ 60
QY 61 QYRVDFKRNKDGINAKVDSIQYDNPNSANIALVYADGEKRIYHCIAPKGLEVGQIVES 120
Db 61 QYRVDFKRDGIGIPGRVATVEYDNPNSANIALVYADGEKRIYHCIAPKGLEVGQIVES 118
QY 121 GAEADTKVGNALPLONIPVGTWVHNIELKPKGGQIARSAGASAOVLGKEGKYVLIRLS 180
Db 119 GENADIKVGNALPLINIPVGTWVHNIELKPKGGQIARSAGASAOVLGKEGKYVLIRLS 178
QY 181 GEVRMILSTCRATIGQVGNLQHELVNKGKRSWKGIPTVRGSGVNNPNDHPHGGGEGR 240
Db 179 GEVRMILSTCRATIGQVGNLQHELVNKGKRSWKGIPTVRGSGVNNPNDHPHGGGEGR 238
QY 241 APGRSPSPMGKPTLGKTKRRGKSSDKLIVRGRKK 278
Db 239 APGRSPSPMGKPTLFTKTRKQKNSDKFIVRRKKNK 276

RESULT 14
RL2_BACHD STANDARD; PRT; 276 AA.
AC Q929L1; Q9JJPY3;
DT 30-MAY-2000 (Rel. 39, Created)
DT 20-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L2.
GN Name=rpL2; OrderedLocusNames=BH0137;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=99209008; PubMed=10192928;
RA Takami H., Takaki Y., Nakasone K., Hirama C., Inoue A., Horikoshi K.;
RT "Sequence analysis of a 32-kb region including the major ribosomal
RT protein gene clusters from alkaliphilic Bacillus sp. strain C-125."
RL Biosci. Biotechnol. Biochem. 63:452-455(1999).
CC [2]
SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -!- FUNCTION: One of the primary rRNA binding proteins. Required for
CC association of the 30S and 50S subunits to form the 70S ribosome,
CC for rRNA binding and peptide bond formation. It has been suggested
CC to have peptidyltransferase activity; this is somewhat
CC controversial. Makes several contacts with the 16S rRNA in the 70S
CC ribosome (By similarity).
CC -!- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the
CC 30S subunit in the 70S ribosome (By similarity).
CC -!- SIMILARITY: Belongs to the ribosomal protein L2P family.
CC -----
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CC -----
CC EMBL; AB017508; BAA75274.1; -;

Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.-D., Errington J., Fabret C., Ferrari A., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Ghim S.Y., Glaeser P., Goffeau A., Golightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
Jones L.-M., Joris B., Karanata D., Kasahara Y., Klaert-Blanchard M.,
Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
Kumano M., Kurita K., Lapidus A., Lardiniois S., Lauber J.,
Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
Scoffone P., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,
Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpestra P.,
Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
Vassarotti A., Viari A., Wamburt R., Wedler E., Wedler H.,
Weitsengger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
Yoshikawa H., Danchin A.,
The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.";
Nature 390:249-256(1997).
-I- FUNCTION: One of the primary rRNA binding proteins. Required for
association of the 30S and 50S subunits to form the 70S ribosome,
for rRNA binding and peptide bond formation. It has been suggested
to have peptidyltransferase activity; this is somewhat
controversial. Makes several contacts with the 16S rRNA in the 70S

```
CC      30S subunit in the 70S ribosome (By similarity).
CC -1- SIMILARITY: Belongs to the ribosomal protein L2p family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation at
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U43929; AAC45959.1; -
DR ENBL; D50302; BAA08834.1; -
DR ENBL; Z99104; CAB11895.1; -
DR PIR; F63694; F63694.
DR HSSP; P04257; IRL2.
DR Subtilist; BG11217; rplB.
DR HAMAP; MF_01320; -, 1.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR002171; Ribosomal_L2.
DR InterPro; IPR005880; Ribosomal_L2_b/O.
DR InterPro; IPR008991; Transl_SH3_like.
DR Pfam; PF00181; Ribosomal_L2; 1.
DR Pfam; PF03947; Ribosomal_L2_C; 1.
DR TIGRFAMs; TIGR01171; rplB_bact; 1.
DR PROSITE; PS00467; RIBOSOMAL_L2; 1.
KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.
FT INIT MET 0 By similarity.
FT FT CONFLICT 115 115 I -> V (in Ref. 2).
FT FT CONFLICT 255 255 E -> G (in Ref. 2).
FT FT CONFLICT 261 261 Q -> K (in Ref. 2).
SQ SEQUENCE 276 AA; 30201 MW; 507B0F524E83A29A CRC64;

Query Match          79.5%; Score 1158; DB 1; Length 276;
Best Local Similarity 79.9%; Pred. No. 1.4e-82;
Matches 222; Conservative 19; Mismatches 35; Indels 2; Gaps 1;

QY      2 AIKKYPITNGRRNWTSLDPAETTKTTTPKSKLLKPKAAGRNNQGKLTVRHGGGKHQR 61
||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
```

CC -!- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the
CC 30S subunit in the 70S ribosome (By similarity).
CC -!- SIMILARITY: Belongs to the ribosomal protein L2P family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AL591983; CAD00707.1; -.
CC PIR; AE1403; AE1403.
CC ListList; LMO02629; -.
CC HAMAP; MF_01320; -; 1.
CC InterPro; IPR002171; Ribosomal_L2.
CC InterPro; IPR005880; Ribosomal_L2_b/o.
CC TIGRFAMs; TIGR01171; rplB_bact; 1.
CC PROSITE; PS00467; RIBOSOMAL_L2; 1.
CC Complete proteome; Ribosomal protein; rRNA-binding; rRNA-binding.
CC SEQUENCE 277 AA; 30505 MW; DD05B498AF5A632 CRC64;
CC -----
Query Match 82.6%; Score 1203; DB 1; Length 277;
Best Local Similarity 82.4%; Pred. No. 4.2e-86;
Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;
QY 1 MAIKYKPTNGRRNMTSLDFAITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGHKKR 60
DB 1 MAIKYKPTNGRRNMTSLDFAITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGHKKR 60
QY 61 QYRVDFKRNKDGINAKVDSIOYDPNRSANIALVYVADGEGKRIYHCIAPKGLEVGQIVRS 120
DB 61 QYRVDFKRNKDGIPGRVATIEYDPNRSANIALINVADGEKR--YIIAAKLEVGQTIVS 118
QY 121 GAADTKVGNALPLQNI PVGTVVHNIELKPGKGGQIARSAGASQVILGKGGKYLRLRS 180
DB 119 GAADIKVGNALPLQNI PVGTVVHNIELKPGKGGQIARSAGTSAQVILGKGGKYLRLRS 178
QY 181 GEVMTLSCTRATIGOVGNLQHELVNKGAGRWGIRPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVMTLATCRATIGOVGNQHELVNKGAGRWGIRPTVRGSMVNPNDHPHGGGEGR 238
QY 241 APIGRSPSPWGKPTLGKTKRRGKSSDKLIIVRGKKK 279
DB 239 APIGRSPSPWGKPTLGKTKRNNNSDKFIVRRKKK 277
RESULT 10
QY1WE9 PRELIMINARY; PRT; 277 AA.
AC QY1WE9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein L2.
GN Name=rplB; OrderedLocusNames=LMOF2365_2602;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RN SEQUENCE FROM N.A.
RP PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Unlich G.A.,
RA Bayles D.O., Luchansky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
RT borne pathogen *Listeria monocytogenes* reveal new insights into the
RT core genome components of this species.";

RL Nucleic Acids Res. 32:2386-2395 (2004).
DR EMBL; AR017331; AAT05367.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0015934; C:large ribosomal subunit; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR008994; Nucleic acid OB.
DR InterPro; IPR002171; Ribosomal_L2.
DR InterPro; IPR005880; Ribosomal_L2_b/o.
DR InterPro; IPR008991; Transl_SH3_like.
DR Pfam; PF00181; Ribosomal_L2; 1.
DR Pfam; PF03947; Ribosomal_L2_C; 1.
DR TIGRFAMs; TIGR01171; rplB_bact; 1.
DR PROSITE; PS00467; RIBOSOMAL_L2; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 277 AA; 30505 MW; DD05B498AF5A632 CRC64;
Query Match 82.6%; Score 1203; DB 2; Length 277;
Best Local Similarity 82.4%; Pred. No. 4.2e-86;
Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;
QY 1 MAIKYKPTNGRRNMTSLDFAITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGHKKR 60
DB 1 MAIKYKPTNGRRNMTSLDFAITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGHKKR 60
QY 61 QYRVDFKRNKDGINAKVDSIOYDPNRSANIALVYVADGEGKRIYHCIAPKGLEVGQIVRS 120
DB 61 QYRVDFKRNKDGIPGRVATIEYDPNRSANIALINVADGEKR--YIIAAKLEVGQTIVS 118
QY 121 GAADTKVGNALPLQNI PVGTVVHNIELKPGKGGQIARSAGASQVILGKGGKYLRLRS 180
DB 119 GAADIKVGNALPLQNI PVGTVVHNIELKPGKGGQIARSAGTSAQVILGKGGKYLRLRS 178
QY 181 GEVMTLSCTRATIGOVGNLQHELVNKGAGRWGIRPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVMTLATCRATIGOVGNQHELVNKGAGRWGIRPTVRGSMVNPNDHPHGGGEGR 238
QY 241 APIGRSPSPWGKPTLGKTKRRGKSSDKLIIVRGKKK 279
DB 239 APIGRSPSPWGKPTLGKTKRNNNSDKFIVRRKKK 277
RESULT 11
QY6PA4 PRELIMINARY; PRT; 277 AA.
AC QY6PA4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE RplB (Ribosomal protein L2) (BL2).
GN Name=rplB; ORFNames=BL01049, BL010136;
OS *Bacillus licheniformis* DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
OX NCBI_TaxID=279010;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=DSM 13;
RC PubMed=15383718;
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
RA Ehrenreich A., Gottschalk G.;
RT "The Complete Genome Sequence of *Bacillus licheniformis* DSM13, an
RT Organism with Great Industrial Potential";
RL J. Mol. Microbiol. Biotechnol. 7:204-211 (2004).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,

RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauguet O.,
RA Entian K.-D., Faihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maltounam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstedt G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.;
RT "Comparative genomics of *Listeria species*";
RL Science 294:849-852(2001).
CC -I- FUNCTION: One of the primary rRNA binding proteins. Required for
CC association of the 30S and 50S subunits to form the 70S ribosome,
CC for rRNA binding and peptide bond formation. It has been suggested
CC to have peptidyltransferase activity; this is somewhat
CC controversial. Makes several contacts with the 16S rRNA in the 70S
CC ribosome (By similarity).
CC -I- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the
CC 30S subunit in the 70S ribosome (By similarity).
CC -I- SIMILARITY: Belongs to the ribosomal protein L2p family.
CC
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CC

RESULTS

RL2 LI5MO STANDARD: PRT: 277 AA.

AC P60426: 0927L0:

DT 29-MAR-2004 (Rel. 43, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation updated)

DE 50S ribosomal protein L2.

GN Name=rp1B; OrderedLocusNames=1mo2629;

OS *Listeria monocytogenes*.

OC Bacteria; Firmicutes; Bacillales; Listeriaceae

OX NCBI_TaxID=1639;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EGD-e / Serovar 1/2a;

RX MEDLINE=21537279; PubMed=11679669; DOI=10.1111/j.1365-2214.2012.02711.x

RA Glaser P., Frangeul L., Buchrieser C., Kusni

KA Baquero F., Berche P., Bloeker H., Brandt F.,

Charbit A., Chetouani F., Couve E., de Larun

RA Domann E., Dominguez-Bernal G., Duchaud E.,
 RA Estacion V. D. Pablin V. Consejo del Pontificio

RA
ENCILIAN K.-D., FBVIM H., GARCIA-DEL FORTILLO
CAUTION I. CASHOL W. COMOT-I ONOT N. UNIN

RA GAUCIER L., GODET W., GOMEZ-LOPEZ N., HALL
PA JONES I., M. KESTER II, KRAFT J, KUBIN M, K

RA JONES D.-M., Kaelin C., Kaelin C.
RA Madhuca E. Maitournam A. Mata Vicente J.

RA Maudeno E., Marcoulam A., Mata Vicente O.,
RA Nordaiek G. Novella S. de Pablos B. Perez

RA Remmel R. Rose M. Schlatter T. Since N.

RA Vazquez-Bol and J.-A. Voss H. Wehland and J. C.

RT "Comparative genomics of *Listeria species*."

RL science 294:849-852(2001).

CC -!- FUNCTION: One of the primary rRNA binding

CC association of the 30S and 50S subunits

CC for tRNA binding and peptide bond format

CC to have peptidyltransferase activity; th

CC controversial. Makes several contacts wi

CC ribosome (By similarity).

Query Match 97.0%; Score 1412; DB 2; Length 277;

Best Local Similarity 98.2%; Pred. No. 1.8e-102;

Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

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QY 1 MAIKKYKPTITNGRRNNTSLDPAEITTKTPEKSLKLPKPKAGRNNOGKLTVRHHGGGCHKR 60
DB 1 MAIKKYKPTITNGRRNNTSLDPAEITTKTPEKSLKLPKPKAGRNNOGKLTVRHHGGGCHKR 60
QY 61 QYRVIDFKRKGKGINAKVDSIQYDNRNSANIALVYVADGKRIYHCHIAPKGLEVGQIVS 120
DB 61 QYRVIDFKRKGKGINAKVDSIQYDNRNSANIALVYVADGKRIYHCHIAPKGLEVGQIVS 118
QY 121 GAEDTKVGNALPLQNI PVGTVVHNI ELKPGKGQIARSAGASAQVLGKGGKTVLRLRS 180
DB 119 GAEDTKVGNALPLQNI PVGTVVHNI ELKPGKGQIARSAGASAQVLGKGGKTVLRLRS 178
QY 181 GEVRMILSTCRATIGQVGNLQHEL VNVGKAGSRWKGI RPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVRMILSTCRATIGQVGNLQHEL VNVGKAGSRWKGI RPTVRGSMVNPNDHPHGGGEGR 238
QY 241 APIGRSPMPGWKPTLGKKTTRGKSSDKLI VGRGKK 279
DB 239 APIGRSPMPGWKPTLGKKTTRGKSSDKLI VGRGKK 277
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RESULT 6

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Q6GEI6 PRELIMINARY; PRT; 277 AA.
AC Q6GEI6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE 50S ribosomal protein L2.
GN Name=rpLb; OrderedLocusNames=SA2332;
OS Staphylococcus aureus (strain MSA252)
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Hollroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Maves R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitz E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG41313.1;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0015934; C:large ribosomal subunit; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR008994; Nucleic acid OB.
DR InterPro; IPR002171; Ribosomal L2.
DR InterPro; IPR005880; Ribosomal L2 b/o.
DR InterPro; IPR008991; Transl SH3 like.
DR Pfam; PF00181; Ribosomal L2; 1.
DR Pfam; PF03947; Ribosomal L2 C; 1.
DR TIGRFAMs; TIGR01171; rplB_bact; 1.
DR PROSITE; PS00467; Ribosomal protein.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 277 AA; 30155 MW; P29296D3EE1E146E CRC64;
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Query Match 97.0%; Score 1412; DB 2; Length 277;

Best Local Similarity 98.2%; Pred. No. 1.8e-102;

Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

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QY 1 MAIKKYKPTITNGRRNNTSLDPAEITTKTPEKSLKLPKPKAGRNNOGKLTVRHHGGGCHKR 60
DB 1 MAIKKYKPTITNGRRNNTSLDPAEITTKTPEKSLKLPKPKAGRNNOGKLTVRHHGGGCHKR 60
QY 61 QYRVIDFKRKGKGINAKVDSIQYDNRNSANIALVYVADGKRIYHCHIAPKGLEVGQIVS 120
DB 61 QYRVIDFKRKGKGINAKVDSIQYDNRNSANIALVYVADGKRIYHCHIAPKGLEVGQIVS 118
QY 121 GAEDTKVGNALPLQNI PVGTVVHNI ELKPGKGQIARSAGASAQVLGKGGKTVLRLRS 180
DB 119 GAEDTKVGNALPLQNI PVGTVVHNI ELKPGKGQIARSAGASAQVLGKGGKTVLRLRS 178
QY 181 GEVRMILSTCRATIGQVGNLQHEL VNVGKAGSRWKGI RPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVRMILSTCRATIGQVGNLQHEL VNVGKAGSRWKGI RPTVRGSMVNPNDHPHGGGEGR 238
QY 241 APIGRSPMPGWKPTLGKKTTRGKSSDKLI VGRGKK 279
DB 239 APIGRSPMPGWKPTLGKKTTRGKSSDKLI VGRGKK 277
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RESULT 7

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RL2_STAEP STANDARD; PRT; 277 AA.
AC Q6CRG3;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L2.
GN Name=rpLb; OrderedLocusNames=SF1821;
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 12228;
RX MEDLINE=22832016; PubMed=12950922;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
RT Staphylococcus epidermidis strain (ATCC 12228).";
RL Mol. Microbiol. 49:1577-1593(2003).
CC -1- FUNCTION: One of the primary rRNA binding proteins. Required for
CC association of the 30S and 50S subunits to form the 70S ribosome,
CC for rRNA binding and peptide bond formation. It has been suggested
CC to have peptidyltransferase activity; this is somewhat
CC controversial. Makes several contacts with the 16S rRNA in the 70S
CC ribosome (By similarity).
CC -1- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the
CC 30S subunit in the 70S ribosome (By similarity).
CC -1- SIMILARITY: Belongs to the ribosomal protein L2p family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AE016750; AAC05462.1;
CC HSSP; P04257; 1RL2.
CC HAMAP; MF 01320; 1.
CC InterPro; IPR008994; Nucleic acid OB.
CC InterPro; IPR002171; Ribosomal L2.
CC InterPro; IPR005880; Ribosomal L2 b/o.
CC InterPro; IPR008991; Transl SH3 like.
CC Pfam; PF00181; Ribosomal L2; 1.
CC Pfam; PF03947; Ribosomal L2 C; 1.
CC TIGRFAMs; TIGR01171; rplB_bact; 1.
CC PROSITE; PS00467; RIBOSOMAL_L2; 1.
```

```
KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.
SQ SEQUENCE 277 AA; 30155 MW; F29296D3EE1E146E CRC64;

Query Match 97.0%; Score 1412; DB 1; Length 277;
Best Local Similarity 98.2%; Pred. No. 1.8e-102;
Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAIKKKYKPIITNGRRNMTSLDFAEITKTTPEKSLKLPKPKAGRNNOGKLTVRHHGGGHR 60
DB 1 MAIKKKYKPIITNGRRNMTSLDFAEITKTTPEKSLKLPKPKAGRNNOGKLTVRHHGGGHR 60
QY 61 QYRVDFPKRNKGINAKVDSIQYDPNRSANIALVYVADGKRIYHCITAPKGLVGQIVS 120
DB 61 QYRVDFPKRNKGINAKVDSIQYDPNRSANIALVYVADGKRIYHCITAPKGLVGQIVS 118
QY 121 GAADTKVGNALPLQNPVGTVVHNIELPKGGOIARSAGASQVLGKGGKYLRLRS 180
DB 119 GAADTKVGNALPLQNPVGTVVHNIELPKGGOIARSAGASQVLGKGGKYLRLRS 178
QY 181 GEVVMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIPTVRGSMNPNNDHPHGGGEGR 240
DB 179 GEVVMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIPTVRGSMNPNNDHPHGGGEGR 238
QY 241 APIGRSPSPMPGKPTLGKTKTRGKSSDKLIVRGRKKK 279
DB 239 APIGRSPSPMPGKPTLGKTKTRGKSSDKLIVRGRKKK 277

RESULT 4
RL2_STAAM STANDARD; PRT; 277 AA.
ID RL2_STAAM AC Q6G774; PRELIMINARY; PRT; 277 AA.
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE 50S ribosomal protein L2.
GN Name=rpL2; OrderedLocusNames=MW2166;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -I- FUNCTION: One of the primary rRNA binding proteins. Required for
association of the 30S and 50S subunits to form the 70S ribosome,
for rRNA binding and peptide bond formation. It has been suggested
to have peptidyltransferase activity; this is somewhat
controversial. Makes several contacts with the 16S rRNA in the 70S
ribosome (By similarity).
CC -I- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the
30S subunit in the 70S ribosome (By similarity).
CC -I- SIMILARITY: Belongs to the ribosomal protein L2P family.
CC -----
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CC -----
CC EMBL; AP004829; BAB96031.1; -.
CC HSSP; P04257; IRL2.
CC HAMAP; MF_01320; -.
CC InterPro; IPR002171; Ribosomal_L2.
CC InterPro; IPR005880; Ribosomal_L2_b/o.
CC TIGRfams; TIGR01171; rplB_bact; 1.
CC PROSITE; PS00467; RIBOSOMAL_L2; 1.
DR
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KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.
SQ SEQUENCE 277 AA; 30155 MW; F29296D3EE1E146E CRC64;

Query Match 97.0%; Score 1412; DB 1; Length 277;
Best Local Similarity 98.2%; Pred. No. 1.8e-102;
Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAIKKKYKPIITNGRRNMTSLDFAEITKTTPEKSLKLPKPKAGRNNOGKLTVRHHGGGHR 60
DB 1 MAIKKKYKPIITNGRRNMTSLDFAEITKTTPEKSLKLPKPKAGRNNOGKLTVRHHGGGHR 60
QY 61 QYRVDFPKRNKGINAKVDSIQYDPNRSANIALVYVADGKRIYHCITAPKGLVGQIVS 120
DB 61 QYRVDFPKRNKGINAKVDSIQYDPNRSANIALVYVADGKRIYHCITAPKGLVGQIVS 118
QY 121 GAADTKVGNALPLQNPVGTVVHNIELPKGGOIARSAGASQVLGKGGKYLRLRS 180
DB 119 GAADTKVGNALPLQNPVGTVVHNIELPKGGOIARSAGASQVLGKGGKYLRLRS 178
QY 181 GEVVMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIPTVRGSMNPNNDHPHGGGEGR 240
DB 179 GEVVMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIPTVRGSMNPNNDHPHGGGEGR 238
QY 241 APIGRSPSPMPGKPTLGKTKTRGKSSDKLIVRGRKKK 279
DB 239 APIGRSPSPMPGKPTLGKTKTRGKSSDKLIVRGRKKK 277

RESULT 5
Q6G774 PRELIMINARY; PRT; 277 AA.
ID Q6G774 AC Q6G774;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE 50S ribosomal protein L2.
GN OrderedLocusNames=SAS2138;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S.G., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CAG43949.1; -.
DR GO; GO:0005822; C:intracellular; IEA.
DR GO; GO:0015934; C:large ribosomal subunit; IEA.
DR GO; GO:0003723; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR002171; Ribosomal_L2.
DR InterPro; IPR005880; Ribosomal_L2_b/o.
DR InterPro; IPR008991; Transl_SH3_like.
DR Pfam; PF00181; Ribosomal_L2; 1.
DR Pfam; PF03947; Ribosomal_L2_C; 1.
DR TIGRfams; TIGR01171; rplB_bact; 1.
DR PROSITE; PS00467; RIBOSOMAL_L2; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 277 AA; 30155 MW; F29296D3EE1E146E CRC64;
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Best Local Similarity 98.2%; Pred. No. 1.8e-102;
Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAIKKYKPTNGRRNMTSLDPAEITKTTPKSKLLKPLPKKAGRNNOGKLTVRHHGGGCHKR 60
DB 1 MAIKKYKPTNGRRNMTSLDPAEITKTTPKSKLLKPLPKKAGRNNOGKLTVRHHGGGCHKR 60

QY 61 QYRVDFPKRKGKINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLVGVQIVES 120
DB 61 QYRVDFPKRKGKINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLVGVQIVES 118

QY 121 GAADTKVGNALPLONIPVGTVVHNIELPKGGOIARSAGASAOVLGKGGKVLRLRS 180
DB 119 GAADTKVGNALPLONIPVGTVVHNIELPKGGOIARSAGASAOVLGKGGKVLRLRS 178

QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRWKGIPTVRGSMVNPNDHPHGGEGR 240
DB 179 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRWKGIPTVRGSMVNPNDHPHGGEGR 238

QY 241 APIGRSPSPMGKPTLGKTKRGGKSSDKLIIVGRKKK 279
DB 239 APIGRSPSPMGKPTLGKTKRGGKSSDKLIIVGRKKK 277

RESULT 2

RL2 STAAU STANDARD; PRT; 277 AA.

ID RL2 STAAU STANDARD; PRT; 277 AA.
AC P60432; Q99S24; Q9AJ03;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L2.
GN Name: rplB; Ordered locus names: S2044;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP MEDLINE=21311952; PubMed=1418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sakimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita N., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
CC -1- FUNCTION: One of the primary RNA binding proteins. Required for
CC association of the 30S and 50S subunits to form the 70S ribosome,
CC for RNA binding and peptide bond formation. It has been suggested
CC to have peptidyltransferase activity; this is somewhat
CC controversial. Makes several contacts with the 16S rRNA in the 70S
CC ribosome (By similarity).
CC -1- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the
CC 30S subunit in the 70S ribosome (By similarity).
CC -1- SIMILARITY: Belongs to the ribosomal protein L2P family.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AP003136; BAB43339.1; -.
CC PIR; B90022; B90022.
CC HSSP; P04257; IRL2.
CC HAMAP; MF 01320; -; 1.
CC InterPro; IPR002171; Ribosomal_L2.
CC DR HAMAP; MF 01320; -; 1.
CC DR InterPro; IPR002171; Ribosomal_L2.
CC DR HAMAP; MF 01320; -; 1.
CC DR InterPro; IPR002171; Ribosomal_L2 b/o.

TIGRFAMS; TIGR01171; rplB_bact; 1.
DR PROSITE; PS00467; RIBOSOMAL_L2; 1.
KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.
SQ SEQUENCE 277 AA; 30155 MW; F29296D3EE1E146E CRC64;

Query Match 97.0%; Score 1412; DB 1; Length 277;
Best Local Similarity 98.2%; Pred. No. 1.8e-102;
Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAIKKYKPTNGRRNMTSLDPAEITKTTPKSKLLKPLPKKAGRNNOGKLTVRHHGGGCHKR 60
DB 1 MAIKKYKPTNGRRNMTSLDPAEITKTTPKSKLLKPLPKKAGRNNOGKLTVRHHGGGCHKR 60

QY 61 QYRVDFPKRKGKINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLVGVQIVES 120
DB 61 QYRVDFPKRKGKINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLVGVQIVES 118

QY 121 GAADTKVGNALPLONIPVGTVVHNIELPKGGOIARSAGASAOVLGKGGKVLRLRS 180
DB 119 GAADTKVGNALPLONIPVGTVVHNIELPKGGOIARSAGASAOVLGKGGKVLRLRS 178

QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRWKGIPTVRGSMVNPNDHPHGGEGR 240
DB 179 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRWKGIPTVRGSMVNPNDHPHGGEGR 238

QY 241 APIGRSPSPMGKPTLGKTKRGGKSSDKLIIVGRKKK 279
DB 239 APIGRSPSPMGKPTLGKTKRGGKSSDKLIIVGRKKK 277

RESULT 3

RL2 STAAU STANDARD; PRT; 277 AA.

ID RL2 STAAU STANDARD; PRT; 277 AA.
AC P60430; Q99S24; Q9AJ03;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L2.
GN Name: rplB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RN6390B;
RA Balaban N.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: One of the primary RNA binding proteins. Required for
CC association of the 30S and 50S subunits to form the 70S ribosome,
CC for RNA binding and peptide bond formation. It has been suggested
CC to have peptidyltransferase activity; this is somewhat
CC controversial. Makes several contacts with the 16S rRNA in the 70S
CC ribosome (By similarity).
CC -1- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the
CC 30S subunit in the 70S ribosome (By similarity).
CC -1- SIMILARITY: Belongs to the ribosomal protein L2P family.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF205220; AAK37412.2; -.
CC HSSP; P04257; IRL2.
CC HAMAP; MF 01320; -; 1.
CC InterPro; IPR002171; Ribosomal_L2.
CC DR InterPro; IPR002171; Ribosomal_L2 b/o.
CC DR TIGRFAMS; TIGR01171; rplB_bact; 1.
CC DR PROSITE; PS00467; RIBOSOMAL_L2; 1.
CC DR HAMAP; MF 01320; -; 1.
CC DR InterPro; IPR002171; Ribosomal_L2.
CC DR HAMAP; MF 01320; -; 1.
CC DR InterPro; IPR002171; Ribosomal_L2 b/o.

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OM protein - protein search, using sw model

Run on: June 9, 2005, 15:49:44 ; Search time 174 Seconds
(without alignments)

821.092 Million cell updates/sec

Title: US-09-839-695B-13

Perfect score: 1456

Sequence: 1 MAIKKYKPTINGRRNWTSLD.....KTRGKSSDKLIVRGKKK 279

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1412	97.0	277	1 RL2_STAAM	P60431 staphylococ
2	1412	97.0	277	1 RL2_STAAM	P60432 staphylococ
3	1412	97.0	277	1 RL2_STAAM	P60430 staphylococ
4	1412	97.0	277	1 RL2_STAAM	P60433 staphylococ
5	1412	97.0	277	2 Q6G774	Q6G774 staphylococ
6	1412	97.0	277	2 Q6G774	Q6G774 staphylococ
7	1373	94.3	277	1 RL2_STAAP	Q8CRG3 staphylococ
8	1203	82.6	277	1 RL2_LISIN	P60425 listeria in
9	1203	82.6	277	1 RL2_LISMO	P60426 listeria mo
10	1203	82.6	277	2 Q71WE9	Q71WE9 listeria mo
11	1175	80.7	277	2 Q65PA4	Q65PA4 bacillus li
12	1158	79.5	276	1 RL2_BACSV	P42919 bacillus su
13	1156	79.4	276	1 RL2_OCEIH	Q8ETX9 oceanobacil
14	1154	79.3	276	1 RL2_BACHD	Q8Z911 bacillus ha
15	1139	78.2	276	1 RL2_BACAN	Q8IVS7 bacillus an
16	1139	78.2	276	2 Q63HB7	Q63HB7 bacillus ce
17	1139	78.2	276	2 Q73F93	Q73F93 bacillus ce
18	1139	78.2	276	2 Q6HP05	Q6HPQ5 bacillus th
19	1137	78.1	276	1 RL2_BACCR	Q81J39 bacillus th
20	1125	77.3	275	1 RL2_BACST	P04257 bacillus st
21	1121	77.0	277	1 RL2_STRF3	Q879r0 streptococ
22	1121	77.0	277	1 RL2_STRF3	P60435 streptococ
23	1121	77.0	277	1 RL2_STRPY	P60434 streptococ
24	1120	76.9	276	1 RL2_ENTFA	Q839g1 streptococ
25	1108	76.1	277	1 RL2_STRPN	Q97sv2 streptococ
26	1108	76.1	277	1 RL2_STRG6	Q8cw5 streptococ
27	1104	75.8	277	1 RL2_STRAS	Q8e7t5 streptococ
28	1104	75.8	277	1 RL2_STRAS	Q8e2c8 streptococ
29	1088	74.7	279	1 RL2_LACPL	Q88xy3 lactobacill
30	1072	73.6	276	1 RL2_LACLA	Q9cdw5 lactococcc
31	1022	70.2	275	1 RL2_THETN	Q8r7v7 thermoanaer

32 1014 69.6 278 2 Q74L86 Q74L86 lactobacill
33 1010 69.4 275 2 Q8GB24 Q8GB24 heliobacill
34 994 68.3 276 1 RL2_ONYPE P60402 onion yello
35 979 67.2 276 1 RL2_ASTYP Q50264 aster yello
36 975.5 67.0 281 1 RL2_MYCHO Q8gm57 mycoplasma
37 969 66.6 277 1 RL2_CLOAB Q97el1 mesoclostridium
38 964.5 66.2 281 2 Q6F121 Q6F121 mesoclostridium
39 962.5 66.1 277 2 Q67JU6 Q67JU6 symbiobacte
40 959 65.9 277 1 RL2_CLOPE Q8xh6 clostridium
41 957 65.7 282 2 Q6MSW8 Q6msm8 mycoplasma
42 956 65.7 278 1 RL2_SPIKU P60404 epioplasma
43 954.5 65.6 283 2 Q6KI52 Q6ki52 mycoplasma
44 924 63.5 276 1 RL2_CLOPE Q890pl clostridium
45 920.5 63.2 281 1 RL2_MYCPU Q98py4 mycoplasma

ALIGNMENTS

RESULT 1

RL2_STAAM STANDARD; PRT; 277 AA.
ID AC P60431; Q99S24; Q9AJ03;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L2.
GN Name=rplB; OrderedLocustNames=SAV2247;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus";
RL Lancel 357:1225-1240 (2001).
CC -!- FUNCTION: One of the primary rRNA binding proteins. Required for
association of the 30S and 50S subunits to form the 70S ribosome,
for rRNA binding and peptide bond formation. It has been suggested
to have peptidyltransferase activity; this is somewhat
controversial. Makes several contacts with the 16S rRNA in the 70S
ribosome (By similarity).
CC -!- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the
30S subunit in the 70S ribosome (By similarity).
CC -!- SIMILARITY: Belongs to the ribosomal protein L2P family.
CC -----
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CC -----
CC EMBL; AP003364; BAB58409.1; -;
DR HSSP; P04257; IRL2.
DR HAMAP; MF 01320; -; 1.
DR InterPro; IPR002171; Ribosomal_L2.
DR InterPro; IPR005880; Ribosomal_L2_b/o.
DR TIGRFAMs; TIGR01171; rplB_bact; 1.
DR PROSITE; PS00467; RIBOSOMAL_L2; 1.
KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.
SQ SEQUENCE 277 AA; 30155 MW; F29296D3EE1E146E CRC64;

Query Match 97.0%; Score 1412; DB 1; Length 277;